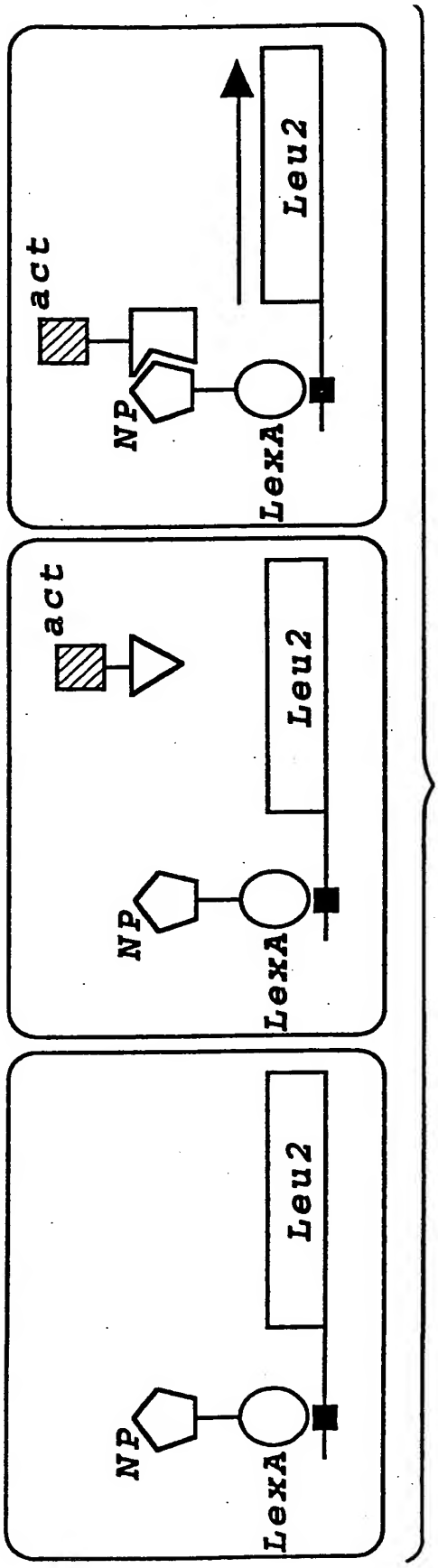

FIG. 1A

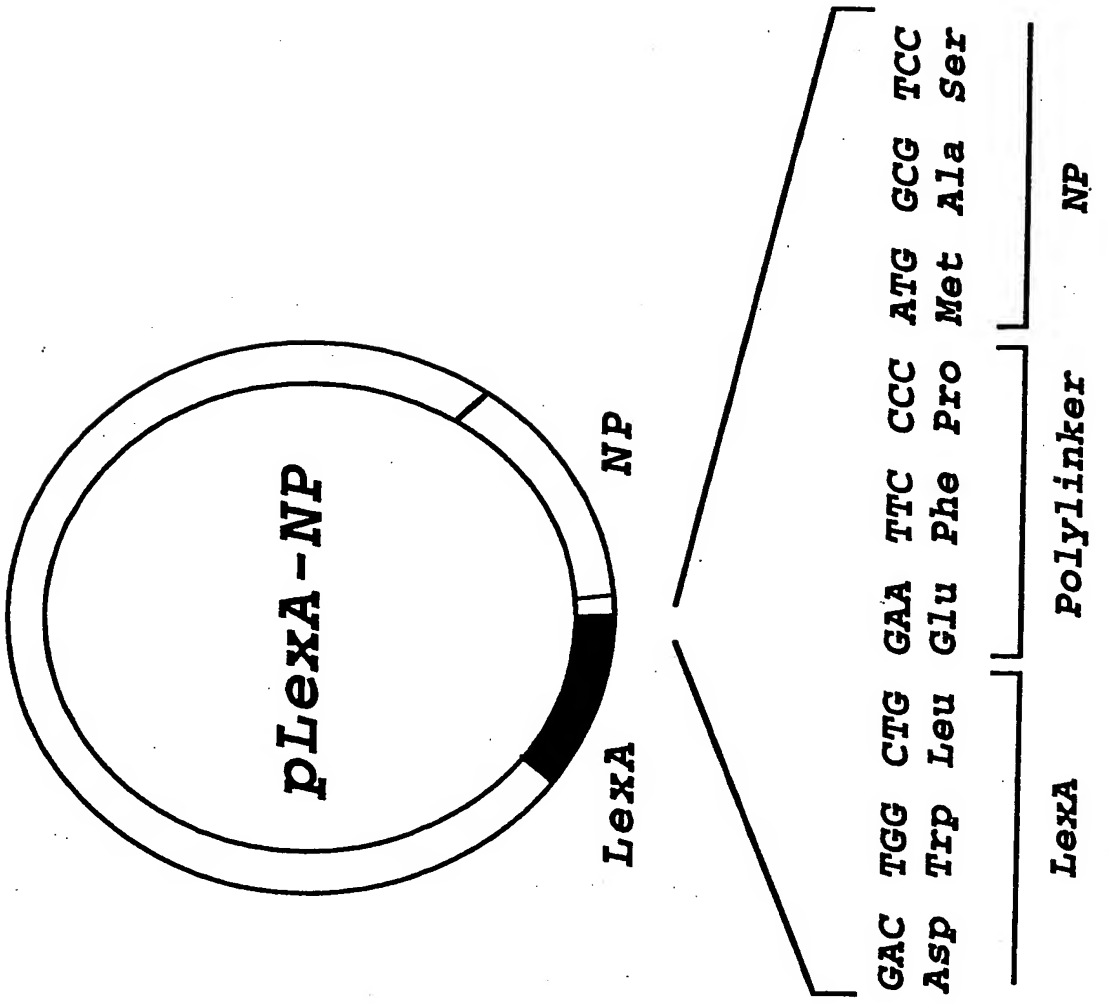
pLexA-NP
LexA
NP
GAC TGG CTG GAA TTC CCC ATG GCG TCC
Asp Trp Leu Glu Phe Pro Met Ala Ser
LexA
Polylinker
NP

FIG. 1B

```
                    20                  40                  60
CTAACTTCAG CGGTGGCACC GGGATCGGTT GCCTTGAGCC TGAAATATGA CCACCCCAGG
                                                  M   T   T   P   G>

                    80                 100                 120
AAAAGAGAAC TTTCGCCTGA AAAGTTACAA GAACAAATCT CTGAATCCCG ATGAGATGCG
  K   E   N   F   R   L   K   S   Y   K   N   K   S   L   N   P   D   E   M   R>

                   140                 160                 180
CAGGAGGAGG GAGGAAGAAG GACTGCAGTT ACGAAAGCAG AAAAGAGAAG AGCAGTTATT
  R   R   R   E   E   E   G   L   Q   L   R   K   Q   K   R   E   E   Q   L   F>

                   200                 220                 240
CAAGCGGAGA AATGTTGCTA CAGCAGAAGA AGAAACAGAA GAAGAAGTTA TGTCAGATGG
  K   R   R   N   V   A   T   A   E   E   E   T   E   E   E   V   M   S   D   G>

                   260                 280                 300
AGGCTTTCAT GAGGCTCAGA TTAGTAACAT GGAGATGGCA CCAGGTGGTG TCATCACTTC
  G   F   H   E   A   Q   I   S   N   M   E   M   A   P   G   G   V   I   T   S>

                   320                 340                 360
TGACATGATT GAGATGATAT TTTCCAAAAG CCCAGAGCAA CAGCTTTCAG CAACACAGAA
  D   M   I   E   M   I   F   S   K   S   P   E   Q   Q   L   S   A   T   Q   K>
```

FIG. 2A

```
                    380                 400                 420
ATTCAGGAAG CTGCTTTCAA AAGAACCTAA CCCTCCTATT GATGAAGTTA TCAGCACACC
  F  R  K   L  L  S   K  E  P  N   P  P  I   D  E  V   I  S  T  P>

                    440                 460                 480
AGGAGTAGTG GCCAGGTTTG TGGAGTTCCT CAAACGAAAA GAGAATTGTT CACTGCAGTT
  G  V  V   A  R  F   V  E  F  L   K  R  K   E  N  C   S  L  Q  F>

                    500                 520                 540
TGAATCAGCT TGGGTACTGA CAAATATTGC TTCAGGAAAT TCTCTTCAGA CCCGAATTGT
  E  S  A   W  V  L   T  N  I  A   S  G  N   S  L  Q   T  R  I  V>

                    560                 580                 600
GATTCAGGCA AGAGCTGTGC CCATCTTCAT AGAGTTGCTC AGCTCAGAGT TTGAAGATGT
  I  Q  A   R  A  V   P  I  F  I   E  L  L   S  S  E   F  E  D  V>

                    620                 640                 660
CCAGGAACAG GCAGTCTGGG CTCTTGGCAA CATTGCTGGA GATAGTACCA TGTGCAGGGA
  Q  E  Q   A  V  W   A  L  G  N   I  A  G   D  S  T   M  C  R  D>

                    680                 700                 720
CTATGTCTTA GACTGCAATA TCCTTCCCCC TCTTTTGCAG TTATTTTCAA AGCAAAACCG
  Y  V  L   D  C  N   I  L  P  P   L  L  Q   L  F  S   K  Q  N  R>
```

FIG. 2B

```
                    740                 760                 780
CCTGACCATG ACCCGGAATG CAGTATGGGC TTTGTCTAAT CTCTGTAGAG GGAAAAGTCC
  L  T  M   T  R  N   A  V  W  A   L  S  N   L  C  R   G  K  S  P>

                    800                 820                 840
ACCTCCAGAA TTTGCAAAGG TTTCTCCATG TCTGAATGTG CTTTCCTGGT TGCTGTTTGT
  P  P  E   F  A  K   V  S  P  C   L  N  V   L  S  W   L  L  F  V>

                    860                 880                 900
CAGTGACACT GATGTACTGG CTGATGCCTG CTGGGCCCTC TCATATCTAT CAGATGGACC
  S  D  T   D  V  L   A  D  A  C   W  A  L   S  Y  L   S  D  G  P>

                    920                 940                 960
CAATGATAAA ATTCAAGCGG TCATCGATGC GGGAGTATGT AGGAGACTTG TGGAACTGCT
  N  D  K   I  Q  A   V  I  D  A   G  V  C   R  R  L   V  E  L  L>

                    980                1000                1020
GATGCATAAT GATTATAAAG TGGTTTCTCC TGCTTTGCGA GCTGTGGGAA ACATTGTCAC
  M  H  N   D  Y  K   V  V  S  P   A  L  R   A  V  G   N  I  V  T>

                   1040                1060                1080
AGGGGATGAT ATTCAGACAC AGGTAATTCT GAATTGCTCA GCTCTGCAGA GTTTATTGCA
  G  D  D   I  Q  T   Q  V  I  L   N  C  S   A  L  Q   S  L  L  H>
```

FIG. 2C

```
                    1100                1120                1140
TTTGCTGAGT AGCCCAAAGG AATCTATCAA AAAGGAAGCA TGTTGGACGA TATCTAATAT
  L  L  S   S  P  K   E  S  I  K   K  E  A   C  W  T   I  S  N  I>

                    1160                1180                1200
TACAGCTGGA AATAGGGCAC AGATCCAGAC TGTGATAGAT GCCAACATTT TCCCAGCCCT
  T  A  G   N  R  A   Q  I  Q  T   V  I  D   A  N  I   F  P  A  L>

                    1220                1240                1260
CATTAGTATT TTACAAACTG CTGAATTTCG GACAAGAAAA GAAGCAGCTT GGGCCATCAC
  I  S  I   L  Q  T   A  E  F  R   T  R  K   E  A  A   W  A  I  T>

                    1280                1300                1320
AAATGCAACT TCTGGAGGAT CAGCTGAACA GATCAAGTAC CTAGTAGAAC TGGGTTGTAT
  N  A  T   S  G  G   S  A  E  Q   I  K  Y   L  V  E   L  G  C  I>

                    1340                1360                1380
CAAGCCGCTC TGTGATCTCC TCACGGTCAT GGACTCTAAG ATTGTACAGG TTGCCCTAAA
  K  P  L   C  D  L   L  T  V  M   D  S  K   I  V  Q   V  A  L  N>

                    1400                1420                1440
TGGCTTGGAA AATATCCTGA GGCTTGGAGA ACAGGAAGCC AAAAGGAACG GCACTGGCAT
  G  L  E   N  I  L   R  L  G  E   Q  E  A   K  R  N   G  T  G  I>
```

FIG. 2D

```
                1460                1480                1500
TAACCCTTAC TGTGCTTTGA TTGAAGAAGC TTATGGTCTG GATAAAATTG AGTTCTTACA
  N  P  Y   C  A  L   I  E  E  A   Y  G  L   D  K  I   E  F  L  Q>

                1520                1540                1560
GAGTCATGAA AACCAGGAGA TCTACCAAAA GGCCTTTGAT CTTATTGAGC ATTACTTCGG
  S  H  E   N  Q  E   I  Y  Q  K   A  F  D   L  I  E   H  Y  F  G>

                1580                1600                1620
GACCGAAGAT GAAGACAGCA GCATTGCACC CCAGGTTGAC CTTAACCAGC AGCAGTACAT
  T  E  D   E  D  S   S  I  A  P   Q  V  D   L  N  Q   Q  Q  Y  I>

                1640                1660                1680
CTTCCAACAG TGTGAGGCTC CTATGGAAGG TTTCCAGCTT TGAAGCAATA CTCTGCTTTC
  F  Q  Q   C  E  A   P  M  E  G   F  Q  L>

                1700                1720                1740
ACGTACCTGT GCTCAGACCA GGCTACCCAG TCGAGTCCTC TTGTGGAGCC CACAGTCCTC

                1760                1780                1800
ATGGAGCTAA CTTCTCAAAT GTTTTCCATA ATACTGTTTG CGCTCATTTG CTTGCCTTGC

                1820                1840                1860
GCACCTGCTC TCTTACACAC ATCTGGAAAA CCTCCGGCTC TCTGTGGTGG GATACCCTTC
```

FIG. 2E

```
                1880                1900                1920
TAATAAAAGG GTAACCAGAA CGGCCCACTC TCTTTTACGG AAAAATCCCT AGGCTTTGGA

                1940                1960                1980
GATCCGCACT TACATTAGAG TTATGGGAAT ATACACATAT TAATGTGGCT CCCTTTTTCT

                2000                2020                2040
TGTGGGGGAA TAAAAGAGGA CTCCTCCTCA TTCCCTTTAA CATGGGGGAA AAAACTGACA

                2060                2080                2100
TTAAAAGATG AGACTAAATC TTTATCTTGA ATTTTACACA ACTACTTACG ACAAGGGAGA

                2120                2140                2160
TGTTTAGACC TGTTGGTATA CTTCAGAGTA CTTTTCATGA GTTCTTCCAC AGTGAACCCT

                2180                2200                2220
TGGATTACCT GGTGGCTTTT TCTAGCCAGA TTGCATTAAT CCTTACTGAG ATTGGATGGT

                2240                2260                2280
TTTCTTTCCT CTATTGGCGC CATTCTTCAG ATATTAAAGT TAAACCATCC ACTCCCTCAC

                2300                2320                2340
CTTCAGCCTT CAGTGAATGT GCTTTCTAGT TGTCAGGAAT GCTGAAGAAT TAACACTTTG
```

FIG. 2F

```
                2360                2380                2400
ACTCCTAAAT GTGATACTGG TGGGTAAGAG CAGGGCACAT TTAATTTGTT CGCTTTTGCT

                2420                2440                2460
TCTCTTTGGT CTGGGCACAT TTAATTTGTT CGCTTTTGCT TCTCTTTGGT CTTTTCGAAT

                2480                2500                2520
ACTTAGTAAT CGAAAACCAT ATCCTGTAAT TTAATAAAAA AAACTAAGGA CGAAAAAACC

                2540                2560                2580
CCTCCAATTT TCCCAAATGC AATCAGTGTA ACTAGGGGCT GTGTTTCTGC ATTAAAATAA

                2600                2620                2640
ATGTTTCAGG CTTTGTGGTC CTGATCAAGG TCCTCATTAA AAAATTGGAG TTCACCCTAG

                2660                2680                2700
GCTTTTCCCC TCTGTGACTG GCAGATAACA CATACTTTTG AAAGTAACTT TGGGATTTTT

                2720                2740                2760
TTTCTTAGGT GCAGCTCGAT TCTAATCTTT TCATGCTGCA CACGATTCCT TTAATCGATA

                2780                2800                2820
GCATCCTTAT CTGAAAGAAA TAACCATCTT CTCAACATGA CCTGCTTAAC CCAAATAAGA
```

FIG. 2G

```
                2840                2860                2880
ACAGTGATCT TATAACCTCA TTGTTTCCTA ATCTATTTTA TTTCATCTCC TGCTAGTACT

                2900                2920                2940
GTGCCGCTTC CCCCTCCCCC CACACAAAAT AAAAACAGTA TCTCGCTTCT GGCTCATTTT
```

FIG. 2H

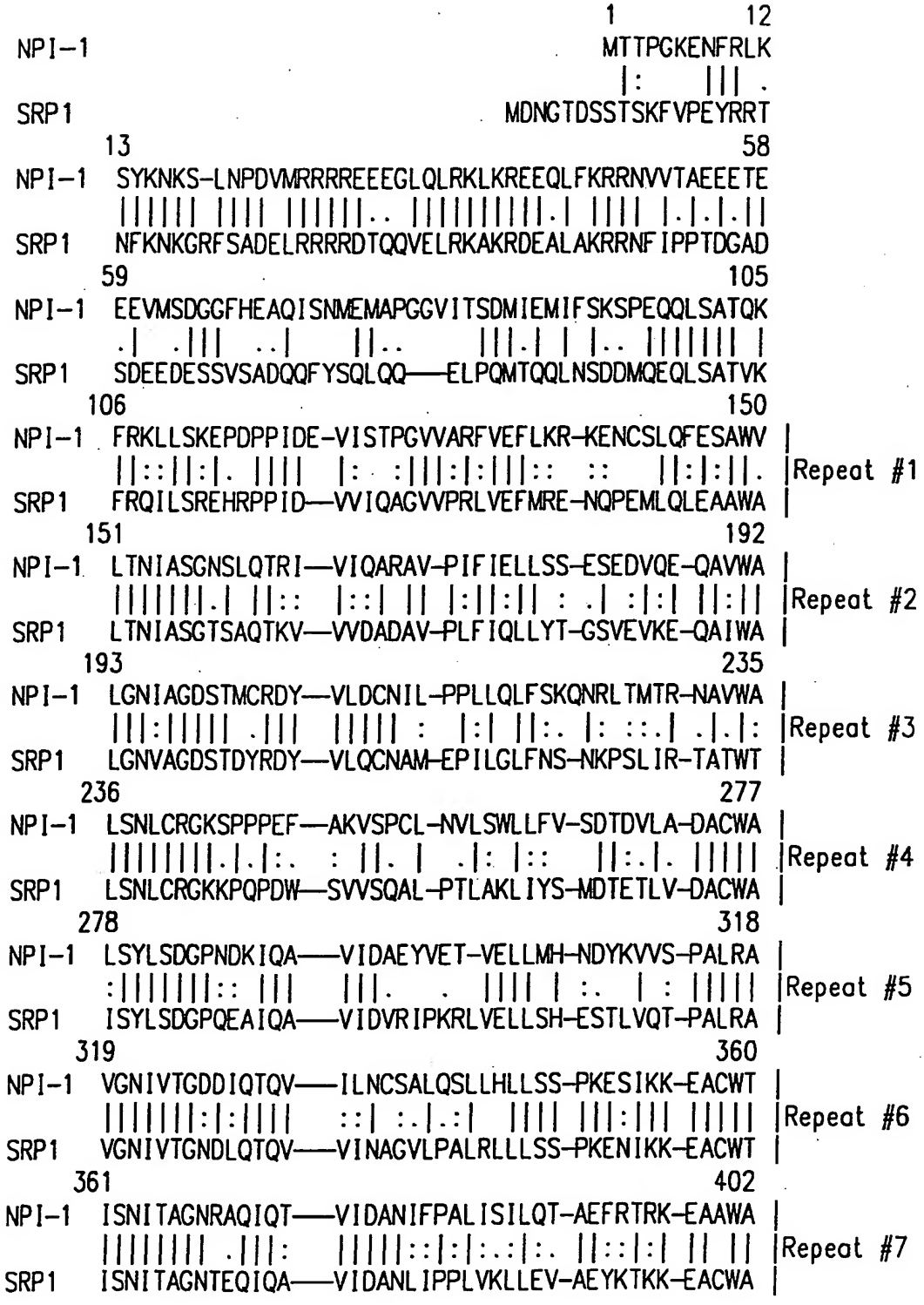
NPI-1 1 MTTPGKENFRLK 12
SRP1 MDNGTDSSTSKFVPEYRRT
NPI-1 13 SYKNKS-LNPDVMRRRREEEGLQLRKLKREEQLFKRRNVVTAEEETE 58
SRP1 NFKNKGRFSADELRRRRDTQQVELRKAKRDEALAKRRNFIPPTDGAD
NPI-1 59 EEVMSDGGFHEAQISNMEMAPGGVITSDMIEMIFSKSPEQQLSATQK 105
SRP1 SDEEDESSVSADQQFYSQLQQ——ELPQMTQQLNSDDMQEQLSATVK
NPI-1 106 FRKLLSKEPDPPIDE-VISTPGVVARFVEFLKR-KENCSLQFESAWV 150
SRP1 FRQILSREHRPPID—VVIQAGVVPRLVEFMRE-NQPEMLQLEAAWA
NPI-1 151 LTNIASGNSLQTRI—VIQARAV-PIFIELLSS-ESEDVQE-QAVWA 192
SRP1 LTNIASGTSAQTKV—VVDADAV-PLFIQLLYT-GSVEVKE-QAIWA
NPI-1 193 LGNIAGDSTMCRDY—VLDCNIL-PPLLQLFSKQNRLTMTR-NAVWA 235
SRP1 LGNVAGDSTDYRDY—VLQCNAM-EPILGLFNS-NKPSLIR-TATWT
NPI-1 236 LSNLCRGKSPPPEF—AKVSPCL-NVLSWLLFV-SDTDVLA-DACWA 277
SRP1 LSNLCRGKKPQPDW—SVVSQAL-PTLAKLIYS-MDTETLV-DACWA
NPI-1 278 LSYLSDGPNDKIQA——VIDAEYVET-VELLMH-NDYKVVS-PALRA 318
SRP1 ISYLSDGPQEAIQA——VIDVRIPKRLVELLSH-ESTLVQT-PALRA
NPI-1 319 VGNIVTGDDIQTQV——ILNCSALQSLLHLLSS-PKESIKK-EACWT 360
SRP1 VGNIVTGNDLQTQV——VINAGVLPALRLLLSS-PKENIKK-EACWT
NPI-1 361 ISNITAGNRAQIQT——VIDANIFPALISILQT-AEFRTRK-EAAWA 402
SRP1 ISNITAGNTEQIQA——VIDANLIPPLVKLLEV-AEYKTKK-EACWA
Repeat #1
Repeat #2
Repeat #3
Repeat #4
Repeat #5
Repeat #6
Repeat #7

FIG.3A

```
     403                                                                445
NPI-1  ITNATSGG—SAEQIKYLVELGCIKPLCDLLTV-MDSKIVQ-VALNG |
       |:||:|||  .:: |:|||. ||||||||||.:  |::|:: |:|:: |Repeat #8
SRP1   ISNASSGGLQRPDIIRYLVSQGCIKPLCDLLEI-ADNRIIE-VTLDA |
     446                                                                490
NPI-1  LENILRLGEQEAKRNGTGINPYCALIEEAYGLDKIEFL-LSHENQEI
       ||||||:||.: . .| .||   .:||.| |::|| |    :||:.|
SRP1   LENILKMGEADKEARGLNINENADFIEKAGGMEKI-FNCQQNENDKI
                                                  ——

     491
NPI-1  YQKAFDLIEHYFGTEDE—DSSIAPQVDLNQQQYIFQQCEAPMEGFQL
       |:||:.:|| |||.|::  |.:::|| . |
SRP1   YEKAYKIIETYFGEEEDAVDETMAPQNAGNTFGFGSNVNQQFNFN

Repeat element Consensuses:
ARM:      L+NLS*+***N+*—ALL**GGL-PALV+LL*S-*+E**L*-*AA*A
              A          II    I    I          I
                         VV    V    V          V

NPI-1
& SRP1:   LSNI*SG***QPQ—*VVI*AGV*PPLV-LL*S-*-*E*K+E-ACWA
          i               V  A
```

FIG.3B

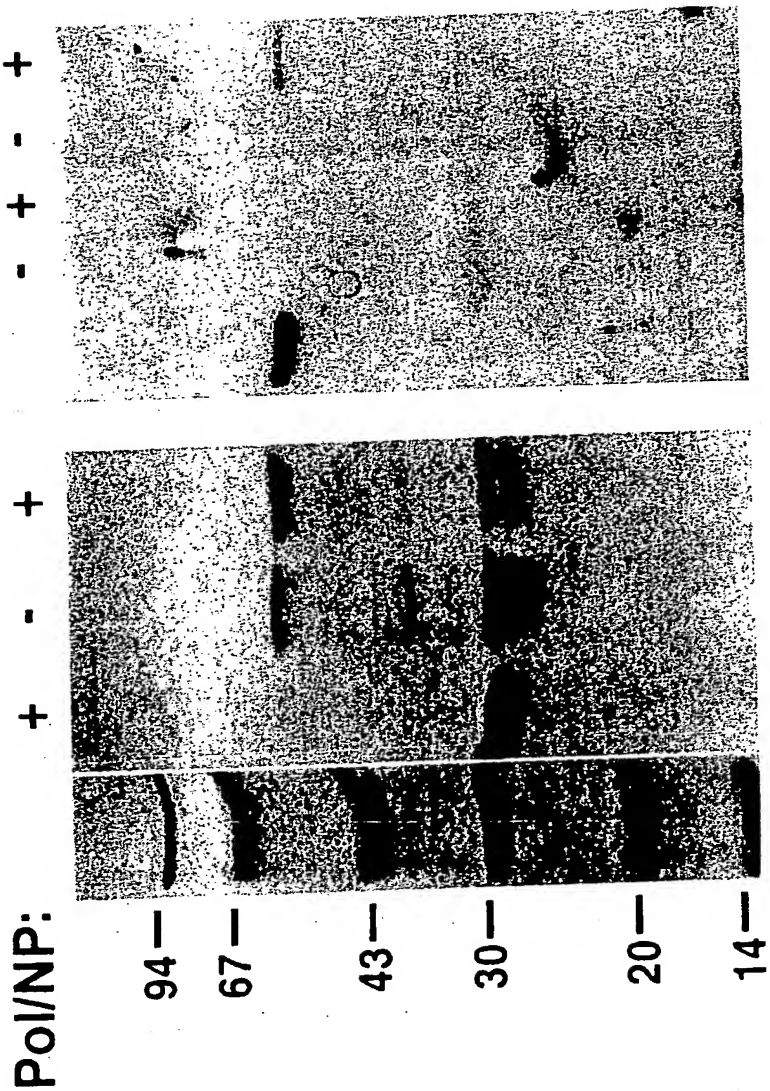

FIG.4

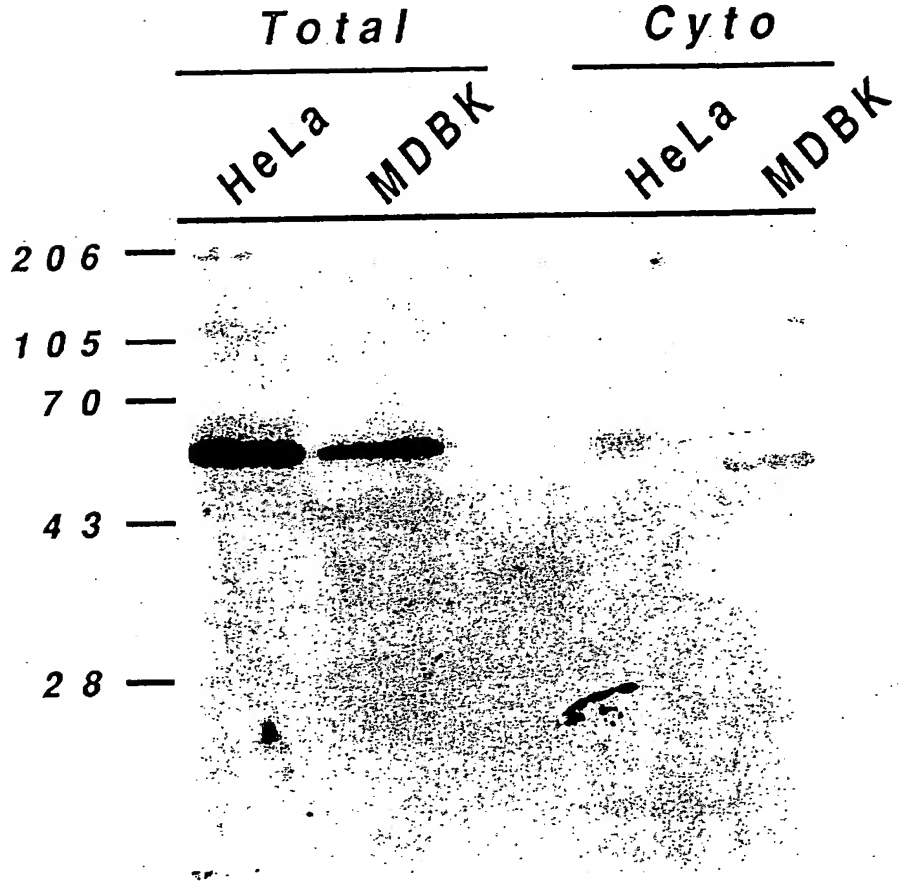

FIG.5

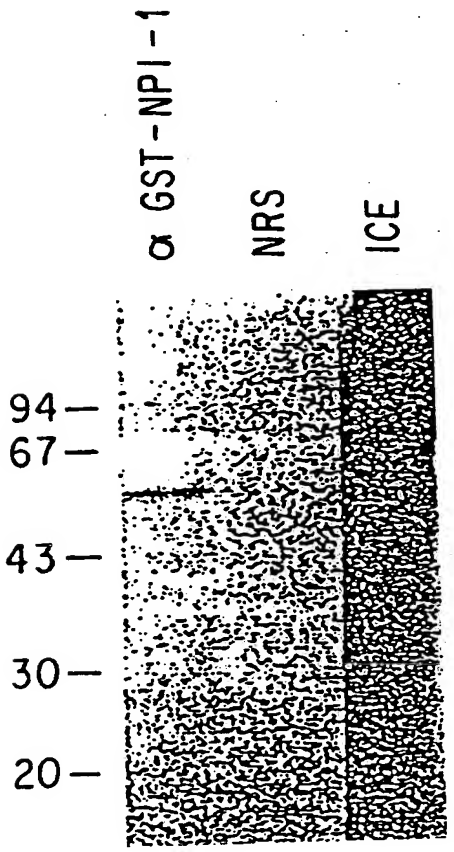

FIG.6

```
                   20                  40                  60
GGAGGCACCG AAGGGCAGCG CCGAGTCGGA GGGGGCGAAG ATTGACGCCA GTAAGAACGA
                   80                 100                 120
GGAGGATGAA GGCCATTCAA ACTCCTCCCC ACGACACTCT GAAGCAGCGA CGGCACAGCG
                  140                 160
GGAAGAATGG AAAATGTTTA TAGGAGGCCT TAGCTGGGAC ACTACAAAGA
```

FIG.7

```
                    20                  40                  60
GAGGTCAATG TGGAGCTGAG GAAAGCTAAG AAGGATGACC AGATGCTGAA GAGGAGAAAT
 E  V  N   V  E  L  R   K  A  K   K  D  D   Q  M  L  K   R  R  N>

                    80                 100                 120
GTAAGCTCAT TTCCTGATGA TGCTACTTCT CCGCTGCAGG AAAACCGCAA CAACCAGGGC
 V  S  S   F  P  D  D   A  T  S   P  L  Q   E  N  R  N   N  Q  G>

                   140                 160                 180
ACTGTAAATT GGTCTGTTGA TGACATTGTC AAAGGCATAA ATAGCAGCAA TGTGGAAAAT
 T  V  N   W  S  V  D   D  I  V   K  G  I   N  S  S  N   V  E  N>

                   200                 220                 240
CAGCTCCAAG CTACTCAAGC TGCCAGGAAA CTACTTTCCA GAGAAAAACA GCCCCCCATA
 Q  L  Q   A  T  Q  A   A  R  K   L  L  S   R  E  K  Q   P  P  I>

                   260                 280                 300
GACAACATAA TCCGGGCTGG TTTGATTCCG AAATTTGTGT CCTTCTTGGG CAGAACTGAT
 D  N  I   I  R  A  G   L  I  P   K  F  V   S  F  L  G   R  T  D>

                   320                 340                 360
TGTAGTCCCA TTCAGTTTGA ATCTGCTTGG GCACTCACTA ACATTGCTTC TGGGACATCA
 C  S  P   I  Q  F  E   S  A  W   A  L  T   N  I  A  S   G  T  S>
```

FIG. 8A

```
                    380                 400                 420
GAACAAACCA AGGCTGTGGT AGATGGAGGT GCCATCCCAG CATTCATTTC TCTGTTGGCA
 E  Q  T   K  A  V  V   D  G  G   A  I  P   A  F  I  S   L  L  A>

                    440                 460                 480
TCTCCCCATG CTCACATCAG TGAACAAGCT GTCTGGGCTC TAGGAAACAT TGCAGGTGAT
 S  P  H   A  H  I  S   E  Q  A   V  W  A   L  G  N  I   A  G  D>

                    500                 520                 540
GGCTCAGTGT TCCGAGACTT GGTTATTAAG TACGGTGCAG TTGACCCACT GTTGGCTCTC
 G  S  V   F  R  D  L   V  I  K   Y  G  A   V  D  P  L   L  A  L>

                    560                 580                 600
CTTGCAGTTC CTGATATGTC ATCTTTAGCA TGTGGCTACT TACGTAATCT TACCTGGACA
 L  A  V   P  D  M  S   S  L  A   C  G  Y   L  R  N  L   T  W  T>

                    620                 640                 660
CTTTCTAATC TTTGCCGCAA CAAGAATCCT GCACCCCCGA TAGATGCTGT TGAGCAGATT
 L  S  N   L  C  R  N   K  N  P   A  P  P   I  D  A  V   E  Q  I>

                    680                 700                 720
CTTCCTACCT TAGTTCGGCT CCTGCATCAT GATGATCCAG AAGTGTTAGC AGATACCTGC
 L  P  T   L  V  R  L   L  H  H   D  D  P   E  V  L  A   D  T  C>
```

FIG. 8B

```
                    740                 760                 780
TGGGCTATTT CCTACCTTAC TGATGGTCCA AATGAACGAA TTGGCATGGT GGTGAAAACA
 W  A  I   S  Y  L  T   D  G  P   N  E  R   I  G  M  V   V  K  T>

                    800                 820                 840
GGAGTTGTGC CCCAACTTGT GAAGCTTCTA GGAGCTTCTG AATTGCCAAT TGTGACTCCT
 G  V  V   P  Q  L  V   K  L  L   G  A  S   E  L  P  I   V  T  P>

                    860                 880                 900
GCCCTAAGAG CCATAGGGAA TATTGTCACT GGTACAGATG AACAGACTCA GGTTGTGATT
 A  L  R   A  I  G  N   I  V  T   G  T  D   E  Q  T  Q   V  V  I>

                    920                 940                 960
GATGCAGGAG CACTCGCCGT CTTTCCCAGC CTGCTCACCA ACCCCAAAAC TAACATTCAG
 D  A  G   A  L  A  V   F  P  S   L  L  T   N  P  K  T   N  I  Q>

                    980                1000                1020
AAGGAAGCTA CGTGGACAAT GTCAAACATC ACAGCCGGCC GCCAGGACCA GATACAGCAA
 K  E  A   T  W  T  M   S  N  I   T  A  G   R  Q  D  Q   I  Q  Q>

                   1040                1060                1080
GTTGTGAATC ATGGATTAGT CCCATTCCTT GTCAGTGTTC TCTCTAAGGC AGATTTTAAG
 V  V  N   H  G  L  V   P  F  L   V  S  V   L  S  K  A   D  F  K>
```

FIG. 8C

```
                    1100                1120                1140
ACACAAAAGG AAGCTGTGTG GGCCGTGACC AACTATACCA GTGGTGGAAC AGTTGAACAG
 T  Q  K   E  A  V  W   A  V  T   N  Y  T   S  G  G  T   V  E  Q>

                    1160                1180                1200
ATTGTGTACC TTGTTCACTG TGGCATAATA GAACCGTTGA TGAACCTCTT AACTGCAAAA
 I  V  Y   L  V  H  C   G  I  I   E  P  L   M  N  L  L   T  A  K>

                    1220                1240                1260
GATACCAAGA TTATTCTGGT TATCCTGGAT GCCATTTCAA ATATCTTTCA GGCTGCTGAG
 D  T  K   I  I  L  V   I  L  D   A  I  S   N  I  F  Q   A  A  E>

                    1280                1300                1320
AAACTAGGTG AAACTAGCTG CCCGTCTTCA CAGATTCAAG AACAAGGGAA AAGACAGTAC
 K  L  G   E  T  S  C   P  S  S   Q  I  Q   E  Q  G  K   R  Q  Y>

                    1340                1360                1380
AGAAATGAGG CGTCCGAGGC GTCGCAGAAT AGAGAAACTT AGTATAATGA TTGAAGAATG
 R  N  E   A  S  E  A   S  Q  N   R  E  T>

                    1400                1420                1440
TGGAGGCTTA GACAAAATTG AAGCTCTACA AAACCATGAA AATGAGTCTG TGTATAAGGC
```

FIG. 8D

```
                1460                1480                1500
TTCGTTAAGC TTAATTGAGA AGTATTTCTC TGTAGAGGAA GAGGAAGATC AAAACGTTGT

                1520                1540                1560
ACCAGAAACT ACCTCTGAAG GCTACACTTT CCAAGTTCAG GATGGGGCTC CTGGGACCTT

                1580                1600                1620
TAACTTTTAG ATCATGTAGC TGAGACATAA ATTTGTTGTG TACTACGTTT GGTATTTTGT

                1640                1660                1680
CTTATTGTTT CTCTACTAAG AACTCTTTCT TAAATGTGGT TTGTTACTGT AGCACTTTTT

                1700                1720                1740
ACACTGAAAC TATACTTGAA CAGTTCCAAC TGTACATACA TACTGTATGA AGCTTGTCCT

                1760                1780                1800
CTGACTAGGT TTCTAATTTC TATGTGGAAT TTCCTATCTT GCAGCATCCT GTAAATAAAC

                1820
ATTCAAGTCC ACCCTTTTCT TGACTTC
```

FIG. 8E

```
                    20                  40                  60
GAACGACCAA GAGGGTGTTC GACTGCTAGA GCCGAGCAGA AGCGTGCCTA AATCAAAGGA

                    80                  100                 120
ACTTGTTTCT TCAAGCTCTT CTGGCAGTGA TTCTGACAGT GAGGTTGACA AAAAGTTAAG

                    140                 160                 180
CAGGAAAAAG CAAGTTGCTC CAGAAAAACC TGTAAAGAAA CAAAAGACAG GTGAGACTTC

                    200                 220                 240
GAGAGCCCTG TCATCTTCTA AACAGAGCAG CAGCAGCAGA GATGATAACA TGTTTCAGAT

TGGGAAAATG AGGTCAGTT
```

FIG.9

```
                    20                  40                  60
TGTCGACTGT GGCTTTGAGC ATCCGTCAGA AGTCCAGCAT GAGTGCATCC CTCAGGCCAT

                    80                  100                 120
TCTGGGAATG GATGTCCTGT GCCAGGCCAA GTCGGGCATG GGAAAGACAG CAGTGTTTGT

                   140                  160                 180
CTTGGCCACA CTGCAACAGC TGGAGCCAGT TACTGGGCAG GTGTCTGTAC TGGTGATGTG

                   200                  220
TCACACTCGG GAGTTGGCTT TTCAGATCAG CAAGGAATAT G
```

FIG. 10

```
                    20                  40                  60
ATTTGTAAAC CCCGGAGCGA GGTTCTGCTT ACCCGAGGCC GCTGCTGTGC GGAGACCCCC

                    80                 100                 120
GGGTGAAGCC ACCGTCATCA TGTCTGACCA GGAGGCAAAA CCTTCAACTG AGGACTTGGG

                   140                 160                 180
GGATAAGAAG GAAGGTGAAT ATATTAAACT CAAAGTCATT GGACAGGATA GCAGTGAGAT

                   200                 220                 240
TCACTTCAAA GTGAAAATGA CAACACATCT CAAGAAACTC AAAGAATCAT ACTGTCAAAG

                   260                 280                 300
ACAGGGTGTT CCAATGAATT CACTCAGGTT TCTCTTTGAG GGTCAGAGAA TTGCTGATAA

                   320                 340                 360
TCATACTCCA AAAGAACTGG GAATGGAGGA AGAAGTTGTG ATTGAAGTTT ATCAGGAACA

AACGGGGGGT CA
```

FIG. 11

```
                                                    -103  TCTGACCCTCGTCCCGCCCCCGC  -80

-81  CATTCGCCGCCTCCTCCTGTCCCGCAGTCGGCGTCCAGCGGCTCTGCTTGTTCGTGTGTGTGTCGTTGCAGGCCTTATTC   -1

1    ATGGGCTCACCGCTGAGGTTCGACGGGCGGGTGGTACTGGTCACCGGCGCGGGGGCAGGATTGGGCCGAGCCTATGCCCT   80
      M  G  S  P  L  R  F  D  G  R  V  V  L  V  T  G  A  G  A  G  L  G  R  A  Y  A  L   27

81   GGCTTTTGCAGAAAGAGGAGCGTTAGTTGTTGTGAATGATTTGGGAGGGGACTTCAAAGGAGTTGGTAAAGGCTCCTTAG  160
       A  F  A  E  R  G  A  L  V  V  V  N  D  L  G  G  D  F  K  G  V  G  K  G  S  L    53

161  CTGATAAGGTTGTTGAAGAAATAAGAAGGAGAGGTGGAAAAGCAGTGGCCAACTATGATTCAGTGGAAGAAGGAGAGAAG  240
      A  D  K  V  V  E  E  I  R  R  R  G  G  K  A  V  A  N  Y  D  S  V  E  E  G  E  K   80

241  GTTGTGAAGACAGCCCTGGATGCTTTTGGAAGAATAGATGTTGTGGTCAACAATGCTGGAATTCTGAGGGATCATTCCTT  320
      V  V  K  T  A  L  D  A  F  G  R  I  D  V  V  V  N  N  A  G  I  L  R  D  H  S  F  107

321  TGCTAGGATAAGTGATGAAGACTGGGATATAATCCACAGAGTTCATTTGCGGGGTTCATTCCAAGTGACACGGGCAGCAT  400
       A  R  I  S  D  E  D  W  D  I  I  H  R  V  H  L  R  G  S  F  Q  V  T  R  A  A   133

401  GGGAACACATGAAGAAACAGAAGTATGGAAGGATTATTATGACTTCATCAGCTTCAGGAATATATGGCAACTTTGGCCAG  480
      W  E  H  M  K  K  Q  K  Y  G  R  I  I  M  T  S  S  A  S  G  I  Y  G  N  F  G  Q  160

481  GCCAATTATAGTGCTGCAAAGTTGGGTCTTCTGGGCCTTGCAAATTCTCTTGCAATTGAAGGCAGGAAAAGCAACATTCA  560
       A  N  Y  S  A  A  K  L  G  L  L  G  L  A  N  S  L  A  I  E  G  R  K  S  N  I  H  187

561  TTGTAACACCATTGCTCCTAATGCGGGATCACGGATGACTCAGACAGTTATGCCTGAAGATCTTGTGGAAGCCTTGAAGC  640
       C  N  T  I  A  P  N  A  G  S  R  M  T  Q  T  V  M  P  E  D  L  V  E  A  L  K   213

641  CAGAGTATGTGGCACCTCTTGTCCTTTGGCTTTGTCACGAGAGTTGTGAGGAGAATGGTGGCTTGTTTGAGGTTGGTGCA  720
      P  E  Y  V  A  P  L  V  L  W  L  C  H  E  S  C  E  E  N  G  G  L  F  E  V  G  A  240
```

FIG. 12A

```
721  GGATGGATTGGAAAATTACGCTGGGAGCGGACTCTTGGAGCTATTGTAAGACAAAAGAATCACCCAATGACTCCTGAGGC  800
       G  W  I  G  K  L  R  W  E  R  T  L  G  A  I  V  R  Q  K  N  H  P  M  T  P  E  A  267

801  AGTCAAGGCTAACTGGAAGAAGATCTGTGACTTTGAGAATGCCAGCAAGCCTCAGAGTATCCAAGAATCAACTGGCAGTA  880
       V  K  A  N  W  K  K  I  C  D  F  E  N  A  S  K  P  Q  S  I  Q  E  S  T  G  S   293

881  TAATTGAAGTTCTGAGTAAAATAGATTCAGAAGGAGGAGTTTCAGCAAATCATACTAGTCGTGCAACGTCTACAGCAACA  960
       I  I  E  V  L  S  K  I  D  S  E  G  G  V  S  A  N  H  T  S  R  A  T  S  T  A  T  320

961  TCAGGATTTGCTGGAGCTATTGGCCAGAAACTCCCTCCATTTTCTTATGCTTATACGGAACTGGAAGCTATTATGTATGC 1040
       S  G  F  A  G  A  I  G  Q  K  L  P  P  F  S  Y  A  Y  T  E  L  E  A  I  M  Y  A  347

1041 CCTTGGAGTGGGAGCGTCAATCAAGGATCCAAAAGATTTGAAATTTATTTATGAAGGAAGTTCTGATTTCTCCTGTTTGC 1120
       L  G  V  G  A  S  I  K  D  P  K  D  L  K  F  I  Y  E  G  S  S  D  F  S  C  L   373

1121 CCACCTTCGGAGTTATCATAGGTCAGAAATCTATGATGGGTGGAGGATTAGCAGAAATTCCTGGACTTTCAATCAACTTT 1200
       P  T  F  G  V  I  I  G  Q  K  S  M  M  G  G  G  L  A  E  I  P  G  L  S  I  N  F  400

1201 GCAAAGGTTCTTCATGGAGAGCAGTACTTAGAGTTATATAAACCACTTCCCAGAGCAGGAAAATTAAAATGTGAAGCAGT 1280
       A  K  V  L  H  G  E  Q  Y  L  E  L  Y  K  P  L  P  R  A  G  K  L  K  C  E  A  V  427

1281 TGTTGCTGATGTCCTAGATAAAGGATCCGGTGTAGTGATTATTATGGATGTCTATTCTTATTCTGAGAAGGAACTTATAT 1360
       V  A  D  V  L  D  K  G  S  G  V  V  I  I  M  D  V  Y  S  Y  S  E  K  E  L  I   453

1361 GCCACAATCAGTTCTCTCTCTTTCTTGTTGGCTCTGGAGGCTTTGGTGGAAAACGGACATCAGACAAAGTCAAGGTAGCT 1440
       C  H  N  Q  F  S  L  F  L  V  G  S  G  G  F  G  G  K  R  T  S  D  K  V  K  V  A  480
```

FIG. 12B

```
1441 GTAGCCATACCTAATAGACCTCCTGATGCTGTACTTACAGATACCACCTCTCTTAATCAGGCTGCTTTGTACCGCCTCAG 1520
      V  A  I  P  N  R  P  P  D  A  V  L  T  D  T  T  S  L  N  Q  A  A  L  Y  R  L  S  507

1521 TGGAGACCGGAATCCCTTACACATTGATCCTAACTTTGCTAGTCTAGCAGGTTTTGACAAGCCCATATTACATGGATTAT 1600
       G  D  R  N  P  L  H  I  D  P  N  F  A  S  L  A  G  F  D  K  P  I  L  H  G  L   533

1601 GTACATTTGGATTTTCTGCCAGGCGTGTGTTACAGCAGTTTGCAGATAATGATGTGTCAAGATTCAAGGCAGTTAAGGCT 1680
      C  T  F  G  F  S  A  R  R  V  L  Q  Q  F  A  D  N  D  V  S  R  F  K  A  V  K  A  560

1681 CGTTTTGCAAAACCAGTATATCCAGGACAAACTCTACAAACTGAGATGTGGAAGGAAGGAAACAGAATTCATTTTCAAAC 1760
      R  F  A  K  P  V  Y  P  G  Q  T  L  Q  T  E  M  W  K  E  G  N  R  I  H  F  Q  T  587

1761 CAAGGTCCAAGAAACTGGAGACATTGTCATTTCAAATGCATATGTGGATCTTGCACCAACATCTGGTACTTCAGCTAAGA 1840
       K  V  Q  E  T  G  D  I  V  I  S  N  A  Y  V  D  L  A  P  T  S  G  T  S  A  K   613

1841 CACCCTCTGAGGGCGGGAAGCTTCAGAGTACCTTTGTATTTGAGGAAATAGGACGCCGCCTAAAGGATATTGGGCCTGAG 1920
      T  P  S  E  G  G  K  L  Q  S  T  F  V  F  E  E  I  G  R  R  L  K  D  I  G  P  E  640

1921 GTGGTGAAGAAAGTAAATGCTGTATTTGAGTGGCATATAACCAAAGGCGGAAATATTGGGGCTAAGTGGACTATTGACCT 2000
      V  V  K  K  V  N  A  V  F  E  W  H  I  T  K  G  G  N  I  G  A  K  W  T  I  D  L  667

2001 GAAAAGTGGTTCTGGAAAAGTGTACCAAGGCCCTGCAAAAGGTGCTGCTGATACAACAATCATACTTTCAGATGAAGATT 2080
       K  S  G  S  G  K  V  Y  Q  G  P  A  K  G  A  A  D  T  T  I  I  L  S  D  E  D   693

2081 TCATGGAGGTGGTCCTGGGCAAGCTTGACCCTCAGAAGGCATTCTTTAGTGGCAGGCTGAAGGCCAGAGGGAACATCATG 2160
      F  M  E  V  V  L  G  K  L  D  P  Q  K  A  F  F  S  G  R  L  K  A  R  G  N  I  M  720

2161 CTGAGCCAGAAACTTCAGATGATTCTTAAAGACTACGCCAAGCTCTGAAGGGCACACTACACTATTAATAAAAATGGAAT 2240
      L  S  Q  K  L  Q  M  I  L  K  D  Y  A  K  L                                    735
```

FIG. 12C

2241 CATTAAATACTCTCTTCACCCAAATATGCTTGATTATTCTGCAAAAGTGATTAGAACTAAGATGCAGGGGAAATTGCTTA 2320

2321 ACATTTTCAGATATCAGATAACTGCAGATTTTCATTTTCTACTAATTTTTCATGTATCATTATTTTTACAAGGAACTATA 2400

2401 TATAAGCTAGCACATAATTATCCTTCTGTTCTTAGATCTGTATCTTCATAATAAAAAAATTTTGCCCAAGTCCTGTTTCC 2480

2481 TTAGAATTTGTGATAGCATTGATAAGTTGAAAGGAAAATTAAATCAATAAAGGCCTTTGATACCTTTAAAAAAAAAAAAA 2560

AAAAAAAAAAAA

FIG. 12D

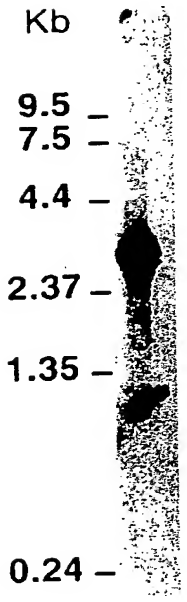

FIG. 13

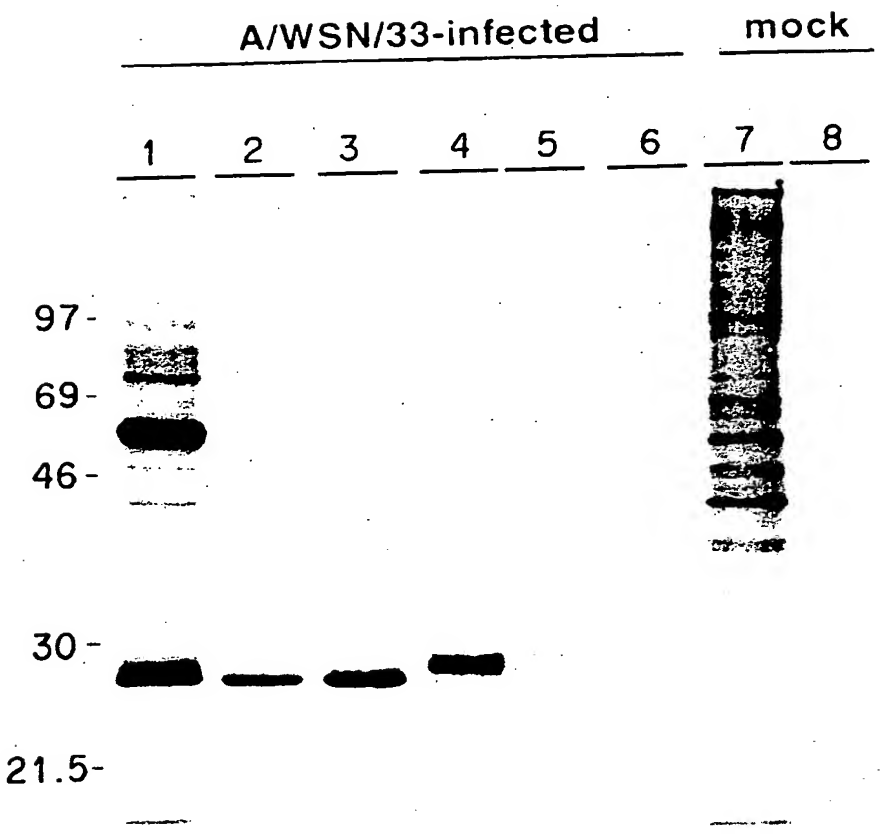

FIG. 14

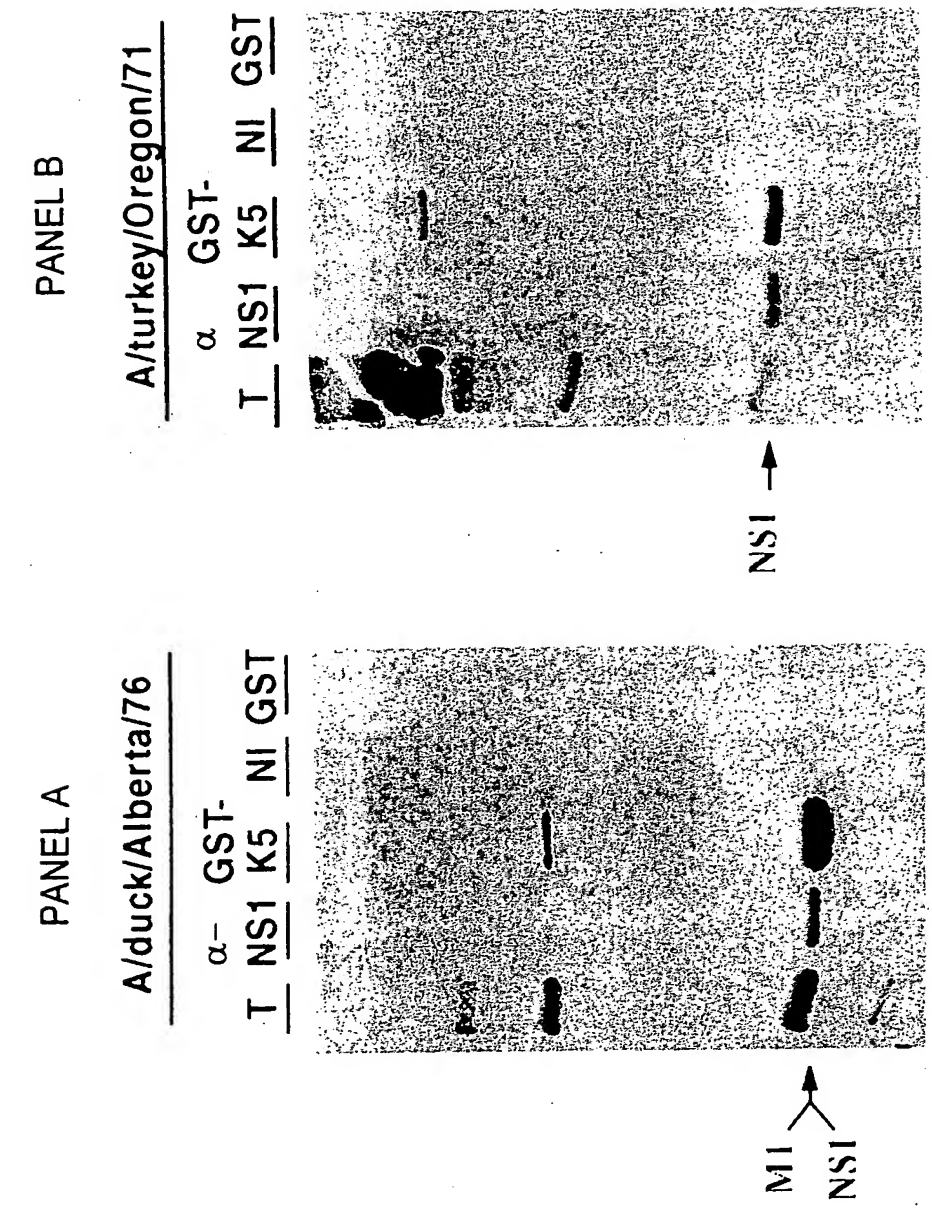

FIG.15B

FIG.15A

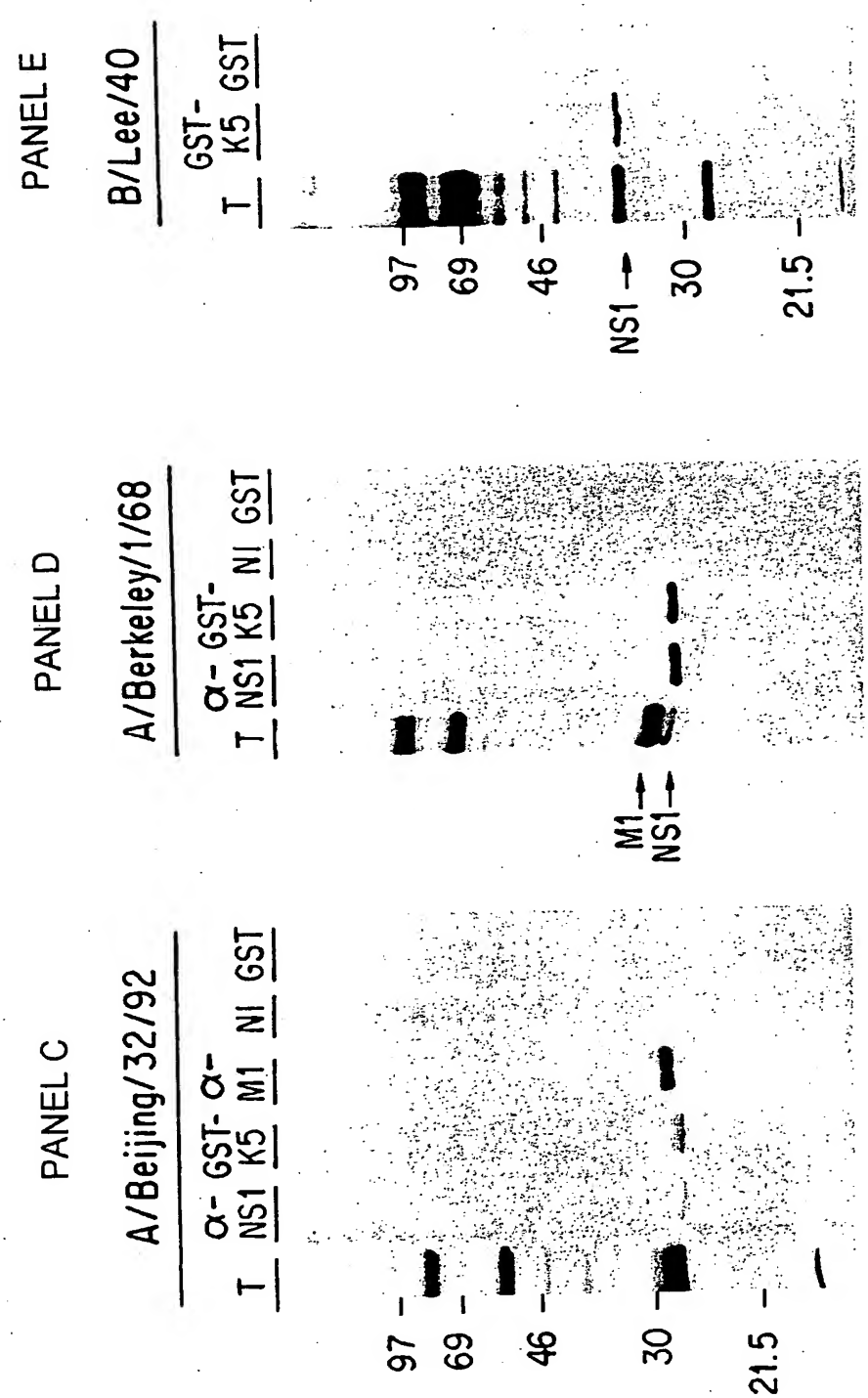

FIG.15C

FIG.15D

FIG.15E

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